

10/588323

253780.txt
SEQUENCE LISTING

JAP20 Rec'd PCT/PTO 03 AUG 2006

<110> Astellas US LLC
MAGILAVY, Daniel

<120> METHODS OF TREATING SKIN DISORDERS

<130> 253780

<150> 60/542,311
<151> 2004-02-06

<150> PCT/US2005/003907
<151> 2005-02-07

<160> 8

<170> PatentIn version 3.3

<210> 1
<211> 753
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(750)

<220>
<221> sig_peptide
<222> (1)..(84)

<220>
<221> misc_feature
<222> (1)..(750)
<223> "Human transmembrane LFA-3"

<220>
<221> mat_peptide
<222> (85)..(750)

<220>
<221> misc_feature
<222> (646)..(646)
<223> "Transmembrane domain"

<400> 1
atg gtt gct ggg agc gac gcg ggg cgg gcc ctg ggg gtc ctc agc gtg 48
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
-25 -20 -15

gtc tgc ctg cac tgc ttt ggt ttc atc agc tgt ttt tcc caa caa 96
Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
-10 -5 -1 1

ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta cca agc aat 144
Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
5 10 15 20

gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat aaa gtt gca 192
Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
25 30 35

253780.txt

gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt aaa aat agg Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg 40 45 50	240
gtt tat tta gac act gtg tca ggt agc ctc act atc tac aac tta aca Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr 55 60 65	288
tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat att act gat Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp 70 75 80	336
acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca tct ccc aca Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr 85 90 95 100	384
cta act tgt gca ttg act aat gga agc att gaa gtc caa tgc atg ata Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile 105 110 115	432
cca gag cat tac aac agc cat cga gga ctt ata atg tac tca tgg gat Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp 120 125 130	480
tgt cct atg gag caa tgt aaa cgt aac tca acc agt ata tat ttt aag Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys 135 140 145	528
atg gaa aat gat ctt cca caa aaa ata cag tgt act ctt agc aat cca Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro 150 155 160	576
tta ttt aat aca aca tca tca atc att ttg aca acc tgt atc cca agc Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser 165 170 175 180	624
agc ggt cat tca aga cac aga tat gca ctt ata ccc ata cca tta gca Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala 185 190 195	672
gta att aca aca tgt att gtg ctg tat atg aat ggt att ctg aaa tgt Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys 200 205 210	720
gac aga aaa cca gac aga acc aac tcc aat tga Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn 215 220	753

<210> 2
<211> 250
<212> PRT
<213> Homo sapiens

<400> 2

Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
-25 -20 -15

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
-10 -5 -1 1

253780.txt

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
5 10 15 20

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
25 30 35

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
40 45 50

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
55 60 65

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
70 75 80

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
85 90 95 100

Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
105 110 115

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
120 125 130

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
135 140 145

Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
150 155 160

Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
165 170 175 180

Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
185 190 195

Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Ile Leu Lys Cys
200 205 210

Asp Arg Lys Pro Asp Arg Thr Asn Ser Asn
215 220

<210> 3
<211> 723
<212> DNA
<213> Homo sapiens

253780.txt

```

<220>
<221> CDS
<222> (1)..(720)

<220>
<221> sig_peptide
<222> (1)..(84)

<220>
<221> misc_feature
<222> (1)..(720)
<223> "Human PI-linked LFA-3"

<220>
<221> mat_peptide
<222> (85)..(720)

<220>
<221> misc_feature
<222> (568)..(720)
<223> "signal sequence for PI-linkage"

<400> 3
atg gtt gct ggg agc gac gcg ggg cgg gcc ctg ggg gtc ctc agc gtg      48
Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
          -25           -20           -15

gtc tgc ctg ctg cac tgc ttt ggt ttc atc agc tgt ttt tcc caa caa      96
Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
          -10            -5            -1   1

ata tat ggt gtt gtg tat ggg aat gta act ttc cat gta cca agc aat      144
Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
5          10           15           20

gtg cct tta aaa gag gtc cta tgg aaa aaa caa aag gat aaa gtt gca      192
Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
          25           30           35

gaa ctg gaa aat tct gaa ttc aga gct ttc tca tct ttt aaa aat agg      240
Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
          40           45           50

gtt tat tta gac act gtg tca ggt agc ctc act atc tac aac tta aca      288
Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
55          60           65

tca tca gat gaa gat gag tat gaa atg gaa tcg cca aat att act gat      336
Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
          70           75           80

acc atg aag ttc ttt ctt tat gtg ctt gag tct ctt cca tct ccc aca      384
Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
85          90           95           100

cta act tgt gca ttg act aat gga agc att gaa gtc caa tgc atg ata      432
Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
          105          110          115

cca gag cat tac aac agc cat cga gga ctt ata atg tac tca tgg gat      480
Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
          120          125          130

```

253780.txt

tgt cct atg gag caa tgt aaa cgt aac tca acc agt ata tat ttt aag Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys 135 140 145	528
atg gaa aat gat ctt cca caa aaa ata cag tgt act ctt agc aat cca Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro 150 155 160	576
tta ttt aat aca aca tca tca atc att ttg aca acc tgt atc cca agc Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser 165 170 175 180	624
agc ggt cat tca aga cac aga tat gca ctt ata ccc ata cca tta gca Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala 185 190 195	672
gta att aca aca tgt att gtg ctg tat atg aat ggt atg tat gct ttt Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe 200 205 210	720
taa	723

<210> 4
<211> 240
<212> PRT
<213> Homo sapiens

<400> 4

Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
-25 -20 -15

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
-10 -5 -1 1

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
5 10 15 20

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
25 30 35

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
40 45 50

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
55 60 65

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
70 75 80

Thr Met Lys Phe Phe Leu Tyr Val Leu Glu Ser Leu Pro Ser Pro Thr
85 90 95 100

253780.txt
Leu Thr Cys Ala Leu Thr Asn Gly Ser Ile Glu Val Gln Cys Met Ile
105 110 115

Pro Glu His Tyr Asn Ser His Arg Gly Leu Ile Met Tyr Ser Trp Asp
120 125 130

Cys Pro Met Glu Gln Cys Lys Arg Asn Ser Thr Ser Ile Tyr Phe Lys
135 140 145

Met Glu Asn Asp Leu Pro Gln Lys Ile Gln Cys Thr Leu Ser Asn Pro
150 155 160

Leu Phe Asn Thr Thr Ser Ser Ile Ile Leu Thr Thr Cys Ile Pro Ser
165 170 175 180

Ser Gly His Ser Arg His Arg Tyr Ala Leu Ile Pro Ile Pro Leu Ala
185 190 195

Val Ile Thr Thr Cys Ile Val Leu Tyr Met Asn Gly Met Tyr Ala Phe
200 205 210

<210> 5
<211> 1056
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1053)

<220>
<221> sig_peptide
<222> (1)..(72)

<220>
<221> misc_feature
<222> (1)..(1053)
<223> "Human CD2"

<220>
<221> mat_peptide
<222> (73)..(1053)

<220>
<221> misc_feature
<222> (628)..(702)
<223> "Transmembrane domain"

<400> 5
atg agc ttt cca tgt aaa ttt gta gcc agc ttc ctt ctg att ttc aat 48
Met Ser Phe Pro Cys Lys Phe Val Ala Ser Phe Leu Leu Ile Phe Asn
-20 -15 -10

gtt tct tcc aaa ggt gca gtc tcc aaa gag att acg aat gcc ttg gaa 96
Val Ser Ser Lys Gly Ala Val Ser Lys Glu Ile Thr Asn Ala Leu Glu

253780.txt

	-5		-1 1		5		
acc tgg ggt gcc ttg ggt cag gac atc aac ttg gac att cct agt ttt							
Thr Trp Gly Ala Leu Gly Gln Asp Ile Asn Leu Asp Ile Pro Ser Phe							
10	15				20		
144							
caa atg agt gat gat att gac gat ata aaa ttg gaa aaa act tca gac							
Gln Met Ser Asp Asp Ile Asp Asp Ile Lys Trp Glu Lys Thr Ser Asp							
25	30				35		
192							
aag aaa aag att gca caa ttc aga aaa gag aaa gag act ttc aag gaa							
Lys Lys Ile Ala Gln Phe Arg Lys Glu Lys Glu Thr Phe Lys Glu							
45	50				55		
240							
aaa gat aca tat aag cta ttt aaa aat gga act ctg aaa att aag cat							
Lys Asp Thr Tyr Lys Leu Phe Lys Asn Gly Thr Leu Lys Ile Lys His							
60	65				70		
288							
ctg aag acc gat gat cag gat atc tac aag gta tca ata tat gat aca							
Leu Lys Thr Asp Asp Gln Asp Ile Tyr Lys Val Ser Ile Tyr Asp Thr							
75	80				85		
336							
aaa gga aaa aat gtg ttg gaa aaa ata ttt gat ttg aag att caa gag							
Lys Gly Lys Asn Val Leu Glu Lys Ile Phe Asp Leu Lys Ile Gln Glu							
90	95				100		
384							
agg gtc tca aaa cca aag atc tcc tgg act tgt atc aac aca acc ctg							
Arg Val Ser Lys Pro Lys Ile Ser Trp Thr Cys Ile Asn Thr Thr Leu							
105	110				115		
120							
acc tgt gag gta atg aat gga act gac ccc gaa tta aac ctg tat caa							
Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln							
125	130				135		
480							
gat ggg aaa cat cta aaa ctt tct cag agg gtc atc aca cac aag tgg							
Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp							
140	145				150		
528							
acc acc agc ctg agt gca aaa ttc aag tgc aca gca ggg aac aaa gtc							
Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val							
155	160				165		
576							
agc aag gaa tcc agt gtc gag cct gtc agc tgt cca gag aaa ggt ctg							
Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu							
170	175				180		
624							
gac atc tat ctc atc att ggc ata tgt gga gga ggc agc ctc ttg atg							
Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu Leu Met							
185	190				195		
200							
gtc ttt gtg gca ctg ctc gtt ttc tat atc acc aaa agg aaa aaa cag							
Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln							
205	210				215		
720							
agg agt cgg aga aat gat gag gag ctg gag aca aga gcc cac aga gta							
Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val							
220	225				230		
768							
gct act gaa gaa agg ggc cgg aag ccc cac caa att cca gct tca acc							
Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr							
235	240				245		
816							
cct cag aat cca gca act tcc caa cat cct cct cca cca cct ggt cat							
Page 7							
864							

253780.txt

Pro	Gln	Asn	Pro	Ala	Thr	Ser	Gln	His	Pro	Pro	Pro	Pro	Pro	Gly	His	
250						255										260
cgt	tcc	cag	gca	cct	agt	cat	cgt	ccc	ccg	cct	cct	gga	cac	cgt	gtt	912
Arg	Ser	Gln	Ala	Pro	Ser	His	Arg	Pro	Pro	Pro	Pro	Gly	His	Arg	Val	
265						270					275					280
cag	cac	cag	cct	cag	aag	agg	cct	cct	gct	ccg	tcg	ggc	aca	caa	gtt	960
Gln	His	Gln	Pro	Gln	Lys	Arg	Pro	Pro	Ala	Pro	Ser	Gly	Thr	Gln	Val	
					285				290					295		
cac	cag	cag	aaa	ggc	ccg	ccc	ctc	ccc	aga	cct	cga	gtt	cag	cca	aaa	1008
His	Gln	Gln	Lys	Gly	Pro	Pro	Leu	Pro	Arg	Pro	Arg	Val	Gln	Pro	Lys	
					300			305					310			
cct	ccc	cat	ggg	gca	gca	gaa	aac	tca	ttg	tcc	cct	tcc	tct	aat	taa	1056
Pro	Pro	His	Gly	Ala	Ala	Glu	Asn	Ser	Leu	Ser	Pro	Ser	Ser	Asn		
						315		320				325				

<210> 6

<211> 351

<212> PRT

<213> Homo sapiens

<400> 6

Met	Ser	Phe	Pro	Cys	Lys	Phe	Val	Ala	Ser	Phe	Leu	Leu	Ile	Phe	Asn
							-20		-15				-10		

Val	Ser	Ser	Lys	Gly	Ala	Val	Ser	Lys	Glu	Ile	Thr	Asn	Ala	Leu	Glu
			-5				-1	1				5			

Thr	Trp	Gly	Ala	Leu	Gly	Gln	Asp	Ile	Asn	Leu	Asp	Ile	Pro	Ser	Phe
10					15					20					

Gln	Met	Ser	Asp	Asp	Ile	Asp	Asp	Ile	Lys	Trp	Glu	Lys	Thr	Ser	Asp
25					30				35			40			

Lys	Lys	Lys	Ile	Ala	Gln	Phe	Arg	Lys	Glu	Lys	Glu	Thr	Phe	Lys	Glu
					45			50				55			

Lys	Asp	Thr	Tyr	Lys	Leu	Phe	Lys	Asn	Gly	Thr	Leu	Lys	Ile	Lys	His
					60			65			70				

Leu	Lys	Thr	Asp	Asp	Gln	Asp	Ile	Tyr	Lys	Val	Ser	Ile	Tyr	Asp	Thr
					75			80			85				

Lys	Gly	Lys	Asn	Val	Leu	Glu	Lys	Ile	Phe	Asp	Leu	Lys	Ile	Gln	Glu
					90			95			100				

Arg	Val	Ser	Lys	Pro	Lys	Ile	Ser	Trp	Thr	Cys	Ile	Asn	Thr	Thr	Leu
105					110				115			120			

253780.txt
Thr Cys Glu Val Met Asn Gly Thr Asp Pro Glu Leu Asn Leu Tyr Gln
125 130 135

Asp Gly Lys His Leu Lys Leu Ser Gln Arg Val Ile Thr His Lys Trp
140 145 150

Thr Thr Ser Leu Ser Ala Lys Phe Lys Cys Thr Ala Gly Asn Lys Val
155 160 165

Ser Lys Glu Ser Ser Val Glu Pro Val Ser Cys Pro Glu Lys Gly Leu
170 175 180

Asp Ile Tyr Leu Ile Ile Gly Ile Cys Gly Gly Ser Leu Leu Met
185 190 195 200

Val Phe Val Ala Leu Leu Val Phe Tyr Ile Thr Lys Arg Lys Lys Gln
205 210 215

Arg Ser Arg Arg Asn Asp Glu Glu Leu Glu Thr Arg Ala His Arg Val
220 225 230

Ala Thr Glu Glu Arg Gly Arg Lys Pro His Gln Ile Pro Ala Ser Thr
235 240 245

Pro Gln Asn Pro Ala Thr Ser Gln His Pro Pro Pro Pro Pro Gly His
250 255 260

Arg Ser Gln Ala Pro Ser His Arg Pro Pro Pro Pro Gly His Arg Val
265 270 275 280

Gln His Gln Pro Gln Lys Arg Pro Pro Ala Pro Ser Gly Thr Gln Val
285 290 295

His Gln Gln Lys Gly Pro Pro Leu Pro Arg Pro Arg Val Gln Pro Lys
300 305 310

Pro Pro His Gly Ala Ala Glu Asn Ser Leu Ser Pro Ser Ser Asn
315 320 325

<210> 7
<211> 1050
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1041)

<220>

253780.txt

<221> sig_peptide
<222> (1)..(84)

<220>
<221> mat_peptide
<222> (85)..(1041)

```
<220>
<221> misc_feature
<222> (85)..(1041)
<223> "LFA3TIP"
```

```
<220>
<221> misc_feature
<222> (360)..(361)
<223> "LFA-3/IgG fusion point"
```

253780.txt

Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	
150					155						160					
gag	gag	cag	tac	aac	agc	acg	tac	cgg	gtg	gtc	agc	gtc	ctc	acc	gtc	624
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	
165					170					175					180	
ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	672
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	
185									190					195		
aac	aaa	gcc	ctc	cca	gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	720
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	
200								205					210			
ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gat	768
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	
215						220						225				
gag	ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	816
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	
230						235				240						
tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	864
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	
245						250				255				260		
aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	tcc	912
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	
265								270					275			
ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	960
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	
280							285						290			
aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	1008
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	
295						300						305				
acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa	tgagtgcgg					1050
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
310						315										

<210> 8
<211> 347
<212> PRT
<213> Homo sapiens

<400> 8

Met Val Ala Gly Ser Asp Ala Gly Arg Ala Leu Gly Val Leu Ser Val
-25 -20 -15

Val Cys Leu Leu His Cys Phe Gly Phe Ile Ser Cys Phe Ser Gln Gln
-10 -5 -1 1

Ile Tyr Gly Val Val Tyr Gly Asn Val Thr Phe His Val Pro Ser Asn
5 10 15 20

253780.txt

Val Pro Leu Lys Glu Val Leu Trp Lys Lys Gln Lys Asp Lys Val Ala
25 30 35

Glu Leu Glu Asn Ser Glu Phe Arg Ala Phe Ser Ser Phe Lys Asn Arg
40 45 50

Val Tyr Leu Asp Thr Val Ser Gly Ser Leu Thr Ile Tyr Asn Leu Thr
55 60 65

Ser Ser Asp Glu Asp Glu Tyr Glu Met Glu Ser Pro Asn Ile Thr Asp
70 75 80

Thr Met Lys Phe Phe Leu Tyr Val Asp Lys Thr His Thr Cys Pro Pro
85 90 95 100

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
105 110 115

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
120 125 130

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
135 140 145

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
150 155 160

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
165 170 175 180

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
185 190 195

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
200 205 210

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
215 220 225

Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
230 235 240

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
245 250 255 260

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
265 270 275

253780.txt

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
280 285 290

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
295 300 305

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
310 315